



02480 U.S.P.T.O.

100303

SEQUENCE LISTING



<110> Skeiky, Yasir
Reed, Steven
Alderson, Mark
Corixa Corporation

<120> Fusion Proteins of *Mycobacterium Tuberculosis*

<130> 014058-009070US

<140> US 09/886,349
<141> 2001-06-20

<150> US 09/597,796
<151> 2000-06-20

<150> US 60/265,737
<151> 2001-02-01

<160> 50

<170> PatentIn Ver. 2.1

<210> 1
<211> 1872
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>

<223> MTB32A (Ra35FL)

<220>

<221> modified_base
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<223> n = g, a, c or t

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ctacaacaac gccgtggcg ccgggacccg catcgtcatc gatcccaacg gtgtcgtgct 360
gaccaacaac cacgtgatcg ccggcgccac cgacatcaat gcgttcaagcg tcggctccgg 420
ccaaacctac ggcgtcgatg tggctggta tgaccgcacc caggatgtcg cgggtctgca 480
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<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB32A (Ra35FL)

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20 25 30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
35 40 45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
50 55 60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65 70 75 80

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
85 90 95

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
100 105 110

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
115 120 125

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
130 135 140

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145 150 155 160

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
165 170 175

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
180 185 190

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
195 200 205

Gly Gly Pro Val Val Asn Gly Leu Gly Gin Val Val Gly Met Asn Thr
 210 215 220

Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225 230 235 240

Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
245 250 255

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
260 265 270

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
275 280 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
290 295 300

Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305 310 315 320

Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
325 330 335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
340 345 350

Pro Pro Ala
355

<210> 3

<211> 1002

<212> DNA

<213> *Mycobacterium tuberculosis*

<220>

<223> MTB32A (Ra35 mature)

<400> 3

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aacatcaaca ccaaactggg ctacaacaac gccgtggcg ccgggaccgg catcgatcatc 180
gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcggccac cgacatcaat 240
gcgttcagcg tcggctccgg ccaaaccatac ggcgtcgatg tggtcggta tgaccgcacc 300
caggatgtcg cggtgctgca gctgcgcggt gccgggtggcc tgccgtcggc ggcgatcggt 360
ggccggcgtcg cgggtggta gcccgtcgct gcgatggca acagcgtgg gcagggcgga 420
acgccccgtg cggtgcttgg cagggtggtc gcgtcgccaa aaccgtgca ggcgtcgat 480
tcgctgaccg gtgccgaaga gacattgaac ggggtgatcc agttcgatgc cgcgatccag 540
cccggtgagg cggggggcc cgtcgtaac ggcttaggac aggtggtcgg tatgaacacg 600
gcccggtccg ataacttcca gctgtccca ggtggcagg gattcgccat tccgatcggt 660
caggcgatgg cgatcgccgg ccagatcgaa tcgggtgggg ggtcaccac cgttcatatc 720
ggccctaccg ctttcctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tccggcgca agtctcgca tctccaccgg cgacgtgatc 840
accgcggtcg acggcgctcc gatcaactcg gccaccgcgta tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcggcgacg cacgcgtaca 960
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<210> 4

<211> 330

<212> PRT

<213> *Mycobacterium tuberculosis*

<220>

<223> MTB32A (Ra35 mature)

<400> 4

Met His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
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Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
20 25 30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
35 40 45

Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
50 55 60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
65 70 75 80

Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
85 90 95

Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
100 105 110

Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val
115 120 125

Val Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val
130 135 140

Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
145 150 155 160

Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
165 170 175

Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
180 185 190

Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
195 200 205

Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
210 215 220

Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly
225 230 235 240

Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
245 250 255

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
260 265 270

Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
275 280 285

Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
290 295 300

Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
305 310 315 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
325 330

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<210> 5
<211> 1002
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Ra35FLMutSA

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ttccccgcgc tgccccctcg a cccgtcccg atggtcgccc aagtggggcc acagggtggc 120
aacatcaaca ccaaactggg ctacaacaac gccgtggcg cccggaccgg catcgatcatc 180
gatccccaaacg gtgtcggtgc gaccaacaac cacgtgatcg cgggcgcccc acatcaat 240
gcgttcagcg tgggtcccg ccaaaccatc ggcgtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cgggtcgatc gctgcgcgg tccgggtggcc tggcgtcgcc ggcgatcggt 360
ggcggcgatcg cgggtggta gcccgtcgac gcatgggca acagcggtgg cagggcgaa 420
acgccccgtg cgggtcgctgg cagggtggtc ggcgtcgatc aaaccgtgca ggcgtcgat 480
tcgtcgaccg gtggcgaaaga gacattgaac ggggtgatcc agttcgatgc cgcgatccag 540
cccggtgtatc cggggcgccg cgtcgatc ggcctaggac aggtggtcgg tatgaacacg 600
gcccgtcccg ataacttcca gctgtcccg ggtggcagg gattcgccat tccgatcgaa 660
caggcgatgg cgatcgccgg ccagatccga tgggtgggg ggtcaccac cgttcatatc 720
gggcctaccg cttctctcg cttgggtgtt gtcgacaaca acggcaacgg cgcacagatc 780
caacgcgtgg tggggagcgc tccggcgca agtctcgatc tctccaccgg cgacgtgatc 840
accgcgtcg acggcgatcc gatcaactcg gccaccggcga tggcgacgc gcttaacggg 900
catatccccg gtgcgtcat ctgggtgacc tggcaaacca agtggggccg cacgcgtaca 960
ggaaacgtga cattggccga gggaccccg gcctgagaat tc 1000

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<210> 6
<211> 330
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Ra35FLMutSA

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Met His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
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Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
30 35 30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
35 40 45

Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
50 55 60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
65 70 75 80

Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
85 90 95

Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 100 105 110
 Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
 115 120 125
 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 130 135 140
 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 145 150 155 160
 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 165 170 175
 Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
 180 185 190
 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 195 200 205
 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 210 215 220
 Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly
 225 230 235 240
 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
 245 250 255
 Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330

<210> 7
 <211> 585
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 7
 gccccgcccgg cttgtcgca ggaccgggttc gcccacttcc ccgcgcgtgcc cctcgaccgg 60
 tccgcgtatgg tcgccaagt gggccacag gtgtcaaca tcaacaccaa actgggctac 120
 aacaacgcccgg tgggcgcgg gaccggcatc gtcatcgatc ccaacgggtgt cgtgctgacc 180
 aacaaccacgg tgatcgccgg cgccaccgac atcaatgcgt tcagcgtcgg ctccggccaa 240
 acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgcgggt gctgcagctg 300
 cgcgggtgccg gtggcctgccc gtcggcggcg atcgggtggcg ggcgtcgcgggt tggtgagccc 360

gtcgtcgca tggcaacag cggtggcag ggccgaacgc cccgtcggt gcctggcagg 420
gtggtcgcgc tcggccaaac cgtgcaggcg tgcgattcgc tgaccgggtc cgaagagaca 480
ttgaacgggt tgatccagtt cgatgcccg atccagcccg gtgaggcggg cgggcccgtc 540
gtcaacggcc taggacaggt ggtcggtatg aacacggccg cgtcc 585

<210> 8
<211> 195
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 8
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
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Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
20 25 30

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
35 40 45

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
50 55 60

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
65 70 75 80

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
85 90 95

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
100 105 110

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
115 120 125

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
130 135 140

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
145 150 155 160

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
165 170 175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
180 185 190

Ala Ala Ser
195

<210> 9
<211> 447
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> Ra12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 9
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caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
cggcgcacgca gtccaaacgcg tggtcggag cgctccggcg gcaagtctcg gcatctccac 240
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cggcgttaac gggcatcata cgggtgacgt catctcggtg aactggcaaa ccaagtgcggg 360
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ataccaccccg cggccggcc aattgga 447

<210> 10
<211> 132
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> Ra 12 or MTBRa12 C-terminus of MTB32A (Ra35FL)

<400> 10
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125

Gly Pro Pro Ala
130

<210> 11
<211> 851
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB39 (TbH9)

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<220>
<221> modified_base
<222> (767)
<223> n = g, a, c or t

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cgccgagaac cgtgctgaac tgatgattct gatagcggacc aacctttgg ggcaaaacac 180
cccgccgatc gcggtcaacg aggccgaata cggcgagatg tggcccaag acgcccggc 240
gatgttggc tacgcccgg cgacggcgc ggcacggcg acgttgctgc cgttcgagga 300
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ctccgacacc gccgcccggc accagttgt gaacaatgtg ccccaggcgc taaaacagtt 420
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gaaacagttac 851

<210> 12
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

<220>
<221> MOD_RES
<222> (254)
<223> Xaa = any amino acid

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Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20 25 30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35 40 45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50 55 60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100 105 110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115 120 125

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Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
 130 135 140
 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 145 150 155 160
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 165 170 175
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 180 185 190
 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
 195 200 205
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220
 Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255
 Arg Arg Asn Gly Gly Pro Ala
 260

<210> 13
 <211> 3058
 <212> DNA
 <213> *Mycobacterium tuberculosis*

 <220>
 <223> MTB39 (TbH9FL)

<400> 13
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 tggcttagc aatggccctg cggcgccccc gacgactggg gtgggtcccc cccgtgcccga 180
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 aggtccgggt tgctgcggcg gcctacgaga cggcgtatgg gctgacggtg ccccgccgg 720
 tgatcgccga gaaccgtgct gaactgtatga ttctgatagc gaccaacccgc ttggggcaaa 780
 acaccccgcc gatcgccgtc aacgaggccg aatacggcga gatgtggcc caagacgccc 840
 cccgcgtt tggctacgcc gccgcgacgg cgcacggcgac ggcgacgtt ctgcccgttc 900
 aggaggcgcc ggagatgacc agcgcgggtg ggctcctcga gcaggccgccc gcggtcgagg 960
 aggctccga caccgcgcgcg gcaaccagt tgatgaacaa tggcccgatgc ggcgtcaac 1020
 agctggccca gcccacgcag ggcaccacgc cttcttccaa gctgggtggc ctgtggaaaga 1080
 cggctcgcc gcacgggtcg ccgatcagca acatgggtgc gatggccaac aaccacatgt 1140
 cgatgaccaa ctgggtgtg tcgtatgacca acacctttag gtcgatgtt aagggttttgc 1200
 ctccggcgcc ggcgcggccag gccgtgcaaa cccgcggcgca aaacgggttc cgggcgatga 1260
 gtcgctggg cagctcgctg gttcttcgg gtcgtggcg gtcgggtggcc gccaacttgg 1320
 gtcggcgcc ctgggtcggt tcgttgcgg tgccgcaggc ctgggcgcg gccaaccagg 1380
 cagtcacccc ggcggcgccg ggcgtgcgcg tgaccagctt gaccagcgcc gcgaaagag 1440

ggcccgggca gatgctggc gggctgcgg tggggcagat gggcgccagg gccgggtgg 1500
 ggctcagtgg tggctgcgt gttccgcgc gaccctatgt gatgccat tctccggcgg 1560
 cccggctagga gagggggcgc agactgtcg tatttgcaca gtgatccggc gtctcggtgt 1620
 ttcccgccgc ggctatgaca acagtcaatg tgcatacggaa gttacaggta ttaggtccag 1680
 gttcaacaag gagacaggca acatggcctc acgtttatg acggatccgc acgcgatgcg 1740
 ggacatggcg ggccgtttt aggtgcacgc ccagacgggt gaggacgagg ctcgcggat 1800
 gtgggcgtcc gcgcaaaaaca tttccgggtc gggctggagt ggcatggcgg aggccaccc 1860
 gctagacacc atggcccaga tgaatcaggc gtttcgcac ac atcgtgaaca tgctgcacgg 1920
 ggtgcgtgac gggctgggtc ggcacgcac caactacggag cagcaagagc aggccctcca 1980
 gcagatccctc agcagctaac gtcagccgtc gcacgcacaa acttttacaa gcgaaaggaga 2040
 acagggttca gtaaccatcaa ctatcaattt gggatgtcg acgctcacgg cgccatgatc 2100
 cgcgctcagg ccgggttgc gggccggag catcaggcca tcattcgtga tgggttgacc 2160
 gcgagtgact tttggggcgg cgccgggtcg ggcgcctgcc aggggttcat taccaggatgg 2220
 gggccgttaact tccagggtat ctacgaggag gccaacgcggc acggggcagaa ggtgcaggg 2280
 gccggcaaca acatggcgca aaccgacagg gcccgcggc ccagctggc ctgacaccag 2340
 gccaaggccca gggacgtggt gtacgaggta agttcctcgc gtgatccctc ggggtggcagt 2400
 ctaagtggtc agtgcgtggg tgggtgggt tggctgttg ggggttctt cgggtgtgg 2460
 cagtgcgtgt cgggctcggt tgaggaccc gaggcccagg tagcgcgtc cttcgatcca 2520
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 gaagatgccc acgacgtcgg ttcggcgtcg tacctctcgg ttgaggcggtt cctgggggtt 2640
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 gccccgggtc tcgaggtgtc cggccaccgc gggaggttt tcggtcagag cgtcgagttac 2760
 ccgatcatat tggcaacaa ctgattcggc gtcggcgtgg tcgtagatgg agtgcagcag 2820
 ggtgcgcacc cacggccagg agggcttcgg gttggctgcc atcagattgg ctgcgttagtg 2880
 ggttctgcag cgctgccagg ccgctgcggg cagggtggcg ccgatcgcgg ccaccaggcc 2940
 ggcgtggcgg tcgctggta ccagcgcac cccggacagg ccgcggcga ccaggtcg 3000
 gaagaacgcc agccagccgg cccgtcctc ggccggagggtg acctggatgc ccaggatc 3058

<210> 14

<211> 391

<212> PRT

<213> *Mycobacterium tuberculosis*

<220>

<223> MTB39 (TbH9FL)

<400> 14

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60

Leu Met Val Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160
 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

<210> 15
 <211> 2287
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:tri-fusion
 protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39
 fusion)

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<220>
<221> CDS
<222> (42)..(2231)
<223> MTB72F

<220>
<221> modified_base
<222> (30)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (33)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (2270)
<223> n = g, a, c or t

<400> 15
tctagaaata attttgttta cttaagaan gatataaca t atg cat cac cat cac 56
Met His His His His
1 5

cat cac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag 104
His His Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln
10 15 20

gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc 152
Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
25 30 35

cga tcg ggt ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc 200
Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe
40 45 50

ctc ggc ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa 248
Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln
55 60 65

cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc 296
Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly
70 75 80 85

gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg 344
Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala
90 95 100

atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg 392
Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val
105 110 115

acc tgg caa acc aag tcg ggc acg cgt aca ggg aac gtg aca ttg 440
Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu
120 125 130

gcc gag gga ccc ccg gcc gaa ttc atg gtg gat ttc ggg gcg tta cca 488
Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro
135 140 145

```

ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser 150 155 160 165	536
ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe 170 175 180	584
tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly 185 190 195	632
tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ser Pro 200 205 210	680
tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala 215 220 225	728
gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu 230 235 240 245	776
acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile 250 255 260	824
ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val 265 270 275	872
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met 280 285 290	920
ttt ggc tac gcc gcg acg gcg acg gcg acg gcg acg ttg ctg ccg Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro 295 300 305	968
ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln 310 315 320 325	1016
gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu 330 335 340	1064
atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag Met Asn Asn Val Pro Gln Ala Leu Gln Leu Ala Gln Pro Thr Gln 345 350 355	1112
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg Gly Thr Thr Pro Ser Ser Lys Leu Gly Leu Trp Lys Thr Val Ser 360 365 370	1160
ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His 375 380 385	1208

atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser 390 395 400 405	1256
atg ttg aag ggc ttt gct ccg gcg gcc cgc cag gcc gtg caa acc Met Leu Lys Gly Phe Ala Pro Ala Ala Arg Gln Ala Val Gln Thr 410 415 420	1304
gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu 425 430 435	1352
ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gac ttg ggt cgg gcg Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala 440 445 450	1400
gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn 455 460 465	1448
cag gca gtc acc ccg gcg cgg gcg ctg ccg ctg acc agc ctg acc Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr 470 475 480 485	1496
agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtc Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val 490 495 500	1544
ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg 505 510 515	1592
gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp 520 525 530	1640
atc gcc ccg ccg gcc ttg tcg cag gac ccg ttc gcc gac ttc ccc gcg Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala 535 540 545	1688
ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtc Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val 550 555 560 565	1736
gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly 570 575 580	1784
acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His 585 590 595	1832
gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly 600 605 610	1880
caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val 615 620 625	1928

gct gtc cgt cgt cgc ggt gcc ggc ctg ccg tcg gct gct atc Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile 630 635 640 645	1976
ggt ggc ggc gtc gct gtt ggt gag ccc gtc gtc gct atg ggc aac agc Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser 650 655 660	2024
ggt ggg cag ggc gga acg ccc cgt gct gtc cct ggc agg gtc gct gct Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala 665 670 675	2072
ctc ggc caa acc gtc cag gct tcc gat tcg ctg acc ggt gcc gaa gag Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu 680 685 690	2120
aca ttg aac ggg ttg atc cag ttc gat gcc gct atc cag ccc ggt gat Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp 695 700 705	2168
tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtc gtc ggt atg aac Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn 710 715 720 725	2216
acg gcc gct tcc tag gatatccatc acactggcgcc cgctcgagc agatccggnt Thr Ala Ala Ser 730	2271
gttacaaagc ccgaaa	2287

<210> 16
 <211> 729
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tri-fusion
 protein MTB72F (Ra12-TbH9-Ra35 or MTB32-MTB39
 fusion)

<400> 16	
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu	
1 5 10 15	
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
20 25 30	
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
85 90 95	
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly	
100 105 110	

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220
 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300
 Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335
 Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Arg
 405 410 415
 Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
435 440 445

Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
450 455 460

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
465 470 475 480

Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
485 490 495

Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
500 505 510

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
515 520 525

Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
530 535 540

Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
545 550 555 560

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
565 570 575

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
580 585 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
595 600 605

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
610 615 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
625 630 635 640

Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
645 650 655

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
660 665 670

Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
675 680 685

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
690 695 700

Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
705 710 715 720

Val Val Gly Met Asn Thr Ala Ala Ser
725

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<210> 17
<211> 2190
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MTB72FMutSA
(Ra12-TbHp-Ra35MutSA) cDNA

<400> 17
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cagggattcg ccattccat cgggcaggcg atggcgatcg cgggcccagat ccgatcgggt 120
gggggtcac ccaccgttca tatcgggctt accgccttcc tcggcttggg tggtgtcgac 180
aacaacggca acggcgcacg agtccaaacgc gtggtcggga ggcgtccggc ggcagaatctc 240
ggcatctcca cccggcgtacgt gatcaccgcg tcgcacggcg ctccgatcaa ctccggccacc 300
gcatggcgg acgcgtttaa cgggcacatcat cccgggtgacg tcatctcggt gacctggcaa 360
accaagtccg gccgcacgcg tacagggaaac gtgacattgg ccgagggacc cccggccgaa 420
ttcatggtg atttcggggc gttaccacccg gagatcaact cccgcaggat gtacggccggc 480
ccgggttcgg cctcgctggc ggcgcggctt cagatgtggg acagcgtggc gagtgacctg 540
tttcggccg cgtccggcgat tcagtcgggt gtcgtgggtc tgacgggtgg gtcgtggata 600
ggtcgtcgat cgggtctgtat ggtggcggcg gcctcgccgt atgtggcgat gatgagcgatc 660
accgcggggc aggccgagct gaccgcgcg caggtccggg ttgctgcggc ggcctacgag 720
acggcgtatg ggctgacggc gccccccgcg gtgatcgccg agaaccgtgc tgaactgtatg 780
attctgtatg cgaccacact cttggggcaa aacaccccg cgcgtccggcgtt caacgaggcc 840
gaatacggcg agatgtggc ccaagacgcg gccgcgtatgt ttggctacgc cgcggcgacg 900
gcgcacggcgat cggcgacgtt gtcgcgttc gaggaggcgc cggagatgac cagcgggggt 960
gggctcctcg agcaggccgc cgcggctcgag gaggcctccg acaccgcgc ggcgaaccag 1020
ttgatgaaca atgtgccccca ggcgctgcaaa cagctggccc agcccacgca gggcaccacg 1080
ccttcttcca agctgggtgg cctgtggaaag acgtctcgatc cgcacatcgatc ggcgtatcagc 1140
aacatgggtcgat cgcgtggccaa caaccacatcg tcgatgacca actcgggtgt gtcgtatgacc 1200
aacacccgtgatc gctcgatgtt gaagggtttt gctccggcg cggccggccca gggctgtcaa 1260
accgcggcgatc aaaacggggcgtatc cgcggcgatc agctcgatgtt gcagctcgatc gggttcttcg 1320
ggtctggcgat gttgggtggc cggcaacttgc ggtcggcgatc ctcggatcgatc ttcgttgcg 1380
gtgcgcggcagg cctggccgcg ggcaaccatc gcagtcaccc cggcggcgatc ggcgtgtccg 1440
ctgaccagcc tcgaccagccgc cgcggaaaga gggccggccg agatgtggg gggcgtgcgc 1500
gtggggcaga tggccggccatc ggcgggtgtt gggctcgtatc gtcgtatcgatc tgggtgtccg 1560
cgaccctatcgat tgcgtccggatc ttctccggatc gccggcgatc tcgccccggc ggccttgcg 1620
caggaccggatc tcgcccactt cccgcgtcgatc cccctcgacc cgtccgcgtatc ggtcgccaa 1680
gtggggccatc aggtggatc catcaacacc aaactgggtt acaacaacgc cgtggggcgcc 1740
gggaccggatc tcgtcatcgatc tcccaacggatc gtcgtatcgatc ccaacaacca cgtatcgatc 1800
ggcgccaccatc acatcaatcgatc gttcagcgatc ggctccggcc aaacctacgg cgtcgatgt 1860
gtcggtatcgat accgcacccatc ggtatgtcgatc gtgtcgatcgatc tgccgcgtgc cgggtggcctg 1920
ccgtccggcgatc cgatcggtgg cggcgatcgatc gttggatcgatc ccgtccgtgc gatggggcaac 1980
agcggtggcgatc agggcgatcgatc gccccgtcgatc gtgcctggatc ggggtggatcgatc gtcggccaa 2040
accgtcgatcgatc cgtccggatcgatc gtcgatcgatc gccgaagatcgatc cattgaacgg gttgatccag 2100
ttcgatcgatc cgatcccgatcgatc cggatcgatcgatc ggccggcccg tcgtcaacgg cctaggacatcgatc 2160
gtggtcgtatc tgaacacggatc cgcgtccctatcgatc 2190

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<210> 18
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MTB72FMutSA
(Ra12-TbHp-Ra35MutSA)

<400> 18
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15

```

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30

Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95

Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125

Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140

Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160

Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
 165 170 175

Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190

Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205

Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220

Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
 225 230 235 240

Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255

Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270

Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285

Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300

Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320

Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335

Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350

Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365

Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380

Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400

Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
 405 410 415

Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala Ala
 435 440 445

Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480

Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495

Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
 500 505 510

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525

Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540

Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640

Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 19
 <211> 1797
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:bi-fusion
 protein TbH9-Ra35 (designated MTB59F)

 <220>
 <221> CDS
 <222> (1)..(1791)
 <223> MTB59F

 <400> 19
 cat atg cat cac cat cac cat cac atg gtg gat ttc ggg gcg tta cca 48
 His Met His His His His His Met Val Asp Phe Gly Ala Leu Pro
 1 5 10 15

 ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg 96
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30

 ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt 144
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45

 tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg 192
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60

 tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg 240
 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65 70 75 80

 tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc 288
 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95

 gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg 336
 Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110

acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att		384	
Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile			
115	120	125	
ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc		432	
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val			
130	135	140	
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg		480	
Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met			
145	150	155	160
ttt ggc tac gcc gcg acg gcg acg gcg acg gcg ttg ctg ccg		528	
Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro			
165	170	175	
ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag		576	
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln			
180	185	190	
gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg aac cag ttg		624	
Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Asn Gln Leu			
195	200	205	
atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag		672	
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln			
210	215	220	
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg		720	
Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser			
225	230	235	240
ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac		768	
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His			
245	250	255	
atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg		816	
Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser			
260	265	270	
atg ttg aag ggc ttt gct ccg gcg gcg gcc cag gcc gtg caa acc		864	
Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr			
275	280	285	
gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg		912	
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu			
290	295	300	
ggt tct tcg ggt ctg ggc ggt ggg gtg gcc aac ttg ggt cgg gcg		960	
Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala			
305	310	315	320
gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac		1008	
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn			
325	330	335	
cag gca gtc acc ccg gcg cgg gcg ctg ccg ctg acc agc ctg acc		1056	
Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr			
340	345	350	

agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val 355 360 365	1104
ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg 370 375 380	1152
gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp 385 390 395 400	1200
atc gcc ccg ccg gcc ttg tcg cag gac ccg ttc gcc gac ttc ccc gcg Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala 405 410 415	1248
ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val 420 425 430	1296
gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly 435 440 445	1344
acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His 450 455 460	1392
gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly 465 470 475 480	1440
caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val 485 490 495	1488
gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile 500 505 510	1536
ggt ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser 515 520 525	1584
ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala 530 535 540	1632
ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu 545 550 555 560	1680
aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp 565 570 575	1728
tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn 580 585 590	1776

acg gcc gcg tcc tag gatatc
Thr Ala Ala Ser
595

1797

<210> 20

<211> 596

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:bi-fusion
protein TbH9-Ra35 (designated MTB59F)

<400> 20

His Met His His His His His Met Val Asp Phe Gly Ala Leu Pro
1 5 10 15

Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
20 25 30

Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
35 40 45

Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
50 55 60

Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65 70 75 80

Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
85 90 95

Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
100 105 110

Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
115 120 125

Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
130 135 140

Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145 150 155 160

Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro
165 170 175

Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
180 185 190

Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Asn Gln Leu
195 200 205

Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
210 215 220

Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225 230 235 240

Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
245 250 255

Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr
 275 280 285
 Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
 290 295 300
 Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Asn
 325 330 335
 Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
 340 345 350
 Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
 355 360 365
 Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg
 370 375 380
 Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
 385 390 395 400
 Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
 405 410 415
 Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
 420 425 430
 Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
 435 440 445
 Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
 450 455 460
 Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
 465 470 475 480
 Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
 485 490 495
 Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
 500 505 510
 Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
 515 520 525
 Gly Gly Gln Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
 530 535 540
 Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
 545 550 555 560
 Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
 565 570 575

Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
580 585 590

Thr Ala Ala Ser
595

<210> 21
<211> 500
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB8.4 (DPV) cDNA

<400> 21
cgtggcaatg tcgttgaccg tcggggccgg ggtcgccctcc gcagatcccg tggacgcgg 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgcgcga cagttcaacg cctcaccggg ggcgcagtcc tatttgcgc atttcctcgc 180
cgcacccgcca cctcagcgcg ctgccatggc cgcgcatttgc caagctgtgc cggggggcggc 240
acagtagacatc ggccttgcg agtcgggttc cggctcctgc aacaactatt aagcccatgc 300
ggggcccatc cgcgcgaccgc gcatcgtcgc cggggctagg ccagatgtcc cgcgtcctca 360
acgggcccga tcccgcgacc cggcattcgtc gccggggcta ggccagattt ccccgctcct 420
caacgggcccgc catctcgtgc cgaattcctg cagccccgggg gatccactag ttctagagcg 480
gccgcccacccg cgggtggagct 500

<210> 22
<211> 96
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB8.4 (DPV)

<400> 22
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15

Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30

Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35 40 45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

<210> 23
<211> 585
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB9.8 (MSL)

<400> 23
tggattccga tagcggtttc ggcccctcga cggcgacca cggcgccgag gcctccgaac 60
ggggggccgg gacgtggg ttcgcccggg ccgcaaccaa agaacgccgg gtccgggcgg 120
tcgggctgac cgcaactggcc ggtgatgagt tcgcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggacgaggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccgtac 300
gggtcgaaaag gagagatgtt atgagcctt tggatgctca tatcccacag ttgggtggcct 360
cccagtccggc gtttgcggcc aaggcggggc tcatgcggca cacgatcggt caggccgagc 420
aggccggcgat gtcggctcag gctttcacc agggggagtc gtcggccggc tttcaggccc 480
cccatgccccg gtttgcggc gccggccgcca aagtcaacac cttgttggat gtcgcgcagg 540
cgaatctggg tgaggccgccc ggtacctatg tggccgccc tgctg 585

<210> 24
<211> 97
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB9.8 (MSL)

<400> 24
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15

Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30

Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35 40 45

Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
50 55 60

Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95

Phe

<210> 25
<211> 1742
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB9.9A (MTI, also known as MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

<400> 25
ccgctcttcaaacgtcat aagttcggtg ggcagtcgg ccgcgcgtgc atatggcacc 60

aataacgcgt gtcccatgga taccggacc gcacgacggt agagcggatc aggcgcagccg 120
 gtggcgaaca ctaccgcgtc cacgctcagc cctggcggtc tgccgaagat cgagcccagg 180
 ttctcatggt cgttaacgac ttccaaacact ggcacgggtgc ggcggccggc gaccacctga 240
 gcaacgcgtcg gtcggcgac ccggcgcgcg gtcgccaaca cccccacgatt gagatggaag 300
 ccgatcaccc gtgccatgac atcagccgac gtcgatagt acggcgccgc gacaccggcc 360
 agatcatcct tgagctcgcc cagccggcg tcggtgcga acagcggccag cggcgtgaac 420
 cgtgaggcca gcatgcgtc caccacccg acaccctcg cgatcaccaa cgccttgcgg 480
 gtcggcagat cgggacnacl gtcgatgtc ttcaaggtcac gggaaatcgtc gagccgtggg 540
 tcgtcggtat cgcagacgtc ctgaacatcg aggccgtcg ggtgctggc acaacggcc 600
 tcggtcacgg gctttcgatc accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
 cacgctcgct gcggttcagc gtcgcgagcc gtcagccag ccacttgc agagagccgt 720
 tgctggatt aattggaga ggaagacagc atgtcgatcg tgaccacaca gccggaagcc 780
 ctggcagctg cggcggcgaa cctacaggtt attggcacga caatgaacgc ccagaacgcg 840
 gccgcggctg ctccaaaccac cggagtagtgc cccgcagccg ccgatgaagt atcagcgtc 900
 accgcggctc agtttgcgtc gcacgcgcag atgtacccaa cggtcagcgc ccaggccgc 960
 gccattcaag aaatgttcgt gaacacgtcg tgccgcgtt ctggctcata cgcggccacc 1020
 gaggcggcca acgcagccgc tgccgcgtga acgggctcg acgaacctgc tgaaggagag 1080
 gggaaacatc cggagttctc gggtcaggggg ttgcgcgcagc gcccagccga ttcaagntatc 1140
 ggcgtccata acagcagacg atctaggcat tcagtaactaa ggagacaggc aacatggcc 1200
 cacgtttat gacggatccg catgcgtatc gggacatggc gggccgttt gaggtgcacg 1260
 cccagacgtt ggaggacgag gtcgcgcggg tggtggcgatc cgcgcacaaac atttccgggt 1320
 cgggctggag tggcatggcc gaggcgaccc cgctagacac catgacttag atgaatcagg 1380
 ctttcgcaa catcgtaac atgctgcacg gggtcgtga cgggctgggt cgcgacgc 1440
 acaantacga acagaacagag caggcctccc agcagatcct gaggcgtatc cgccgaaagc 1500
 cacagctngt tacgnnttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
 cggggacgtc gacgctcatg ggcgcgtatg cccgcgtcag gcccgcgtc ttgaggcggg 1620
 gcatcaggcc atcgatcgatc atgtgttggc cgggggtgac ttttggggcg gcccgggttc 1680
 ggtggcttgc caggagttca ttaccgcgtt gggccgtaa ttccaggtga tctacgagca 1740
 gg 1742

<210> 26
 <211> 2836
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> MTB9.9A (MTI also known as MTI-A)

<220>
 <221> modified_base
 <222> (104)
 <223> n = g, a, c or t

<400> 26
 gtgtattccg ttgcggcgc cggcgaagac caccaactcc gctgggtgg tcgcacaggc 60
 ggttgcgtcg gtcagctggc cgaatccaa tgattgggtgg ctctngtgcgg ttgtgggtc 120
 cgattacccc cacggaaagg acgacgtatcg ttctgttgcg cggtcagtcg tacttggcga 180
 cgggcatggc gcggtttctt acctcgatcg cacagcagct gacccgcgc ccagggggca 240
 caacggctgg ctccggcgga gcctggtacc caacgcacca attcgcgcgc ctgggtgcag 300
 gcccggcggt gtcggcgagt ttggcgcggt cggagccgtt cgggaggttgc tgggtgcgc 360
 caagttgggc cgtcgccgtt ccggccttcg cggagaagcc tgaggcgggc acggcgtatgt 420
 ccgtcatcggt cgaagcgatcc agctcggtc agggaggccct gcttcgaggc ataccgttgc 480
 cgagagcggtt gcccgcgtaca ggcgccttcg ctcaccgata cgggtttccgc cacagcgtga 540
 ttaccgggtc tccgtcgccg ggtatagctt cgtatccggc tgcgcgcgc cccgaaatgc 600
 tgcagatagc gatcgaccgc gcccgtcgatc aaacgcgcac cacggcacta tcaatgcgc 660
 cggcggcggt tgatgccaat ttgaccgtcc cgacggggct ttatctgcgg caagatttca 720
 tccccagccc ggtcggtggg ccgataaaata cgctgggtcag cgcgactt cccgctgaat 780
 tcgtatcgatc gggcgccgc tcgacgcgcgatc gtatctcgatc tggggcccaa accccgtcaa 840
 acgctgttac tggcggttac ccacagggtga atttgcgggtc ccaactgggtg aacacttgcg 900
 aacgggtggc atcgaaatca acttgcgtcg ttgcgtatgt ctactctt ccaacttgcg 960

gttgctggga ttaattggga gaggaagaca gcatgtcggt cgtgaccaca cagccggaag 1020
 ccctggcagc tgcggcgccg aacctacagg gtattggcac gacaatgaac gcccagaacg 1080
 cggccgcggc tgctccaacc accggagtag tgcccgcagc cgccgatgaa gtatcagcgc 1140
 tgaccgcggc tcagtttgcg ggcacacgc agatgtacca aacggtcagc gcccaggccg 1200
 cggccatcca cgaaatgttc gtgaacacgc tggtgccag ttctggctca tacgcggcca 1260
 cggaggcggc caacgcagcc gtcgceggct gAACGGGCTC gcacgaacct gctgaaggag 1320
 agggggaaaca tccggagttc tcgggtcagg gttgcgcca gcccagcc gattcagcta 1380
 tcggcgtcca taacacgaga cgatctaggc attcagtact aaggagacag gcaacatggc 1440
 ctcacgtttt atgacggatc cgcatcgat gcgggacatg gcgggcccgtt ttgaggtgca 1500
 cggccagacg gtggaggacg aggctcgccg gatgtggcg tccgcgaaa acatttccgg 1560
 tgcgggctgg agtggcatgg ccgaggcgac ctcgctagac accatgaccc agatgaatca 1620
 ggcgttgc aacatcgta acatgctca cggggctgg gacgggctgg ttgcgcacgc 1680
 caacaactac gaacacgaa acgggcctc ccagcagatc ctgagcagct agcgcggaaa 1740
 gcccacagctg cgtacgctt ctcacattag gagaacacca atatgacgat taattaccag 1800
 ttcggggacg tcgacgctca tggcgccatg atccgcgtc aggccgcgtc gcttgaggcg 1860
 gagcatcagg ccacgttcg tgatgtttt gcccgggtg actttttggg cggcgccgg 1920
 tcggtggtt gccaggagtt cattaccag ttggccgtt aacttceaggt gatctacgag 1980
 caggccaacg cccacggca gaaggtgcag gtcgcccga acaacatggc gcaaaaccgac 2040
 agcgcgcgtc gtcacgctg ggcctaaac tgaacttcag tcgcggcagc acaccaacca 2100
 gccgggtgtc tgctgtgtcc tgcaagttaac tagcactcgat ccgctgaggt agcgatggat 2160
 caacagagta cccgcaccga catcaccgtc aacgtcgacg gcttctggat gcttcaggcg 2220
 ctactggata tccggccacgt tgccgtcgag ttacgttgcg gggcgtaacgt ctccaccgt 2280
 tccaatgact ggctaaacga gcacccgggg atggcgtca tgccgcgagca gggcattgtc 2340
 gtcaacgacg cggtaaacga acaggtcgct gcccggatga aggtgcttgc cgccacctgat 2400
 cttgaagtctg tcgcccgtc gtcacgcggc aagttgtctgt acgggggtcat agacgacgag 2460
 aaccagccgc cgggttcgcg tgacatccct gacaatgagt tccgggtgg gttggcccg 2520
 cgaggccagc actgggtgtc ggcggtaacgg gttggcaatg acatcaccgt cgatgacgt 2580
 acgggtctcg atagccctc gatcgccgca ctgtaatgg acgggtctgga gtcgattcac 2640
 cacgcccacc cagccgcgtat caacgcggc aacgtgcca tggaggagat ctgcgtccg 2700
 attcggcacc aggcacgagg cgggtgtcggt gacgacggga tcgatcacga tcatcgaccg 2760
 gccgggatcc ttggcgatct cgtttagac gaccggggcc cgcggaaagc tctgcgacat 2820
 ccatgggttc ttcccc 2836

<210> 27

<211> 94

<212> PRT

<213> *Mycobacterium tuberculosis*

<220>

<223> MTB9.9A (MTI, also known as MTI-A) ORF peptide

<400> 27

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met

1 5 10 15

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 28
<211> 1200
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB40 (HTCC#1) cDNA

<400> 28
caggcatgag cagagcggttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gatttggaaa cccaaaccaag ggggtatcct ttactcctca ctagagttact 120
tcgaaaaaagc cctggaggag ctggcagcag cgtttccggg tggatggctgg ttaggttcgg 180
ccgcggacaa atacgcccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
actctcgatcg tcagtcgtatc agcctgtatcc acgaccaggc caacgcggtc cagacgacc 300
gacgacatccgt ggagggcgcc aagaaaggc tcgagttcgt ggcggccgtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tattcggccgc cttccaggcg ccgtttgcg 420
cgggcgcgat ggccgttagtgc ggcggcgcgc ttgcctactt ggtcgtaaa acgctgtatca 480
acgcgactca actccctcaaa ttgcttggca aatttggcgga gttggtcgcg gccgcattt 540
cgacatcatat ttccggatgtg gccggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgcgtcaac ggcctgaaag agctttggga caagctcactg ggttgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagttcctt ctttgcggc gtccccggct 720
tgaccggcgc gaccaggcgc ttgtcgcaag tgacttggctt gttcggtgcg gccggctgt 780
ccgcacatcgatc gggcttggct cacggata ggcctggcgc gtcagccgc ttgccccggcc 840
tggccggcat tggggggcggt tccggttttt ggggcttggcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgtatgg cccggcgcgc gccgctgcgc 960
agcagggtcgg cgggcagtcg cagctggctt ccgcgcaggg ttcccaaggt atgggcggac 1020
ccgttaggcat gggcggcatg caccctctt cggggggcgatc gaaaggagcg accacgaaga 1080
agtaactcgga aggcgcggcg gcgccactg aagacgcccga ggcgcgcgc gtcgaagctg 1140
acgcggggcg tggggcaaaag gtgctggtaa gaaacgtcgt ctaacggcat ggcgagccaa 1200

<210> 29
<211> 392
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> MTB40 (HTCC#1)

<400> 29
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

<210> 30
 <211> 1441
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
<223> MTB41 (MTCC#2) cDNA

<400> 30
gaggttgctg gcaatggatt tcgggcttt acctccggaa gtgaattcaa gccgaatgta 60
ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctggacg gtgtggccgc 120
ggagttgact tccggccggg tctcgatgg atcgggtggg tcgacgctga tcgttgagcc 180
gtggatgggg ccggcggcgg ccgcgatggc ggccgcggca acgcccgtatg tgggggtggct 240
ggccgcacag gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaaagc 300
gtttgggacg gcgttgcgta tgacgggtgcc accatccctc gtcgcggcca accgcagccg 360
gttgatgtcg ctgggtcgccg cgaacattct gggcaaaaac agtgcggcga tcgcggctac 420
ccaggcccgag tatgccgaaa tggggccca agacgctgcc gtgatgtaca gctatgaggg 480
ggcatctgcg gccgcgtccgg cgttgcgcgc gttcaactca cccgtgcaag gcaccggccc 540
ggccggggccc gcggccgcag ccgcggcgcac ccaagccgccc ggtgcggcgc ccgttgcgga 600
tgcacaggcg acactggcccc agctgcccc gggatcctg agcgacattc tgcggcatt 660
ggccgcacac gctgatccgc tgacatccgg actgttgggg atcgcgtcga ccctcaaccc 720
gcaagtcgga tccgctcagc cgatagtat ccccaccccg atagggaaat tggacgtat 780
cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctcgcgatca cgaacacggc 840
cagaccctgg cacatcgcc tatacggaa cgcggccggg ctgggaccga cgcaggggcca 900
tccactgagt tcggcgaccg acgagccgg gcccactgg ggcgccttcg ggggcgcggc 960
gccgggtgtcc gcgggcgtcg gccacgcgcg attagtcgga gcttgcgcg tgccgcacag 1020
ctggaccacg gccgcggccgg agatccagct cgcgcgttcag gcaacacccca cttcagctc 1080
cagcgccggc gccgacccga cggccctaaa cggatgccc gcaggcctgc tcagcgggat 1140
ggcttggcg agcctggccg cacgcggcac gacgggcggt ggcggcaccc gtagcggcac 1200
cagcaactgac gccaagagg acggccgcaa acccccggtt gttgtattt gagaagcagcc 1260
gccgcggcga aaccccccgc ggtaaaagtc cggcaaccgt tcgtcggcgc gccgaaaatg 1320
cctggtgagc gtggctatcc gacgggcgt tcacaccgt ttagtagtgct tacggctatg 1380
gacgacggtg tctggattct cggcgctat cagagcgatt ttgctcgcaa cctcagcaaa 1440
g 1441

<210> 31
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 31
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
1 5 10 15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
20 25 30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
35 40 45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
50 55 60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
65 70 75 80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala
85 90 95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
100 105 110

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

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<210> 32
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 32
atgacagagc agcagtggaa tttcgcggtt atcgaggccg cggcaagcgc aatccaggg 60
aatgtcacgt ccattcattc ctccttgcac gaggggaaagc agtccctgac caagctcgca 120
gcggcctggg gcggttagcgg ttccggaaagcg tacc 154

<210> 33
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 33
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45

Glu Ala Tyr
50

<210> 34
<211> 327
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Tb38-1 or 38-1 (MTb11)

<400> 34
cggcacgaga gaccgatgcc gctaccctcg cgcaaggaggc aggttaatttc gagcggatct 60
ccggcgacct gaaaacccag atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120
agtggcgcgg cgcggcgaaa acggccgccc agggccgcgtt ggtgcgttc caagaagcag 180
ccaataagca gaagcaggaa ctcgacgaga tctcgacgaa tattcgtcag gcccggcgtcc 240
aataactcgag ggccgacgag gaggcagcagc aggcgcgtgc ctcgcaaatg ggcttctgac 300
ccgctaatac gaaaagaaac ggagcaa 327

<210> 35
<211> 95
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Tb38-1 or 38-1 (MTb11)

```

```

<400> 35
Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20 25 30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35 40 45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50 55 60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65 70 75 80

Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85 90 95

```

```

<210> 36
<211> 542
<212> DNA
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbRa3

```

```

<220>
<221> modified_base
<222> (406)
<223> n = g, a, c or t

```

```

<400> 36
gaattcggca cgagaggta tcgacatcat cgggaccagc cccacatcct gggAACAGGC 60
ggcggcggag gcggtccagc gggcgcgaga tagcgtcgat gacatcccg gtcgtcggt 120
cattgagca gacatggccg tggacagcgc cggcaagatc acctaccgca tcaagctcg 180
agtgtcggtc aagatgaggc cggcgcaacc ggcgtacac gggccggcga gcaagacgca 240
aaatcgacg .gtttcggtt gattcgtcg attttgtgtc tgctcgccga ggcctaccag 300
gcccggccca ggtccgcgtc ctgcccgtatc caggcgtgca tcgcgattcc ggcggccacg 360
ccggagttaa tgcttcgcgt cggccgtaaac tggcgatcc gccggngagc tgcgtcgat 420
ccgtggccag cccgtcgatg cccgagttgc cggaggaaac gtgcgtccag gccggtagga 480
acgtccgt a ggcggcggtc ctgaccggct ctgcctgcgc cctcagtgcg gccagcgagc 540
gg 542

```

```

<210> 37
<211> 66
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbRa3

```

```

<400> 37
Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1 5 10 15

Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20 25 30

```

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35 40 45

Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50 55 60

Pro Arg
65

<210> 38
<211> 1993
<212> DNA
<213> *Mycobacterium tuberculosis*

<220>
<223> 38 kD

<400> 38

tgttcttcga cggcaggctg gtggaggaag ggcccaccga acagctgttc tcctcgccga 60
agcatgcgga aaccgcccga tacgtcggc gactgtcggg ggacgtcaag gacgccaagc 120
gccccaaattt aagagcacag aaaggtatgg cgtgaaaatt cggttgcata cgctgttggc 180
cggttgcacc gctgcgcccgc tgctgcttagc agccggccggc tggctcga aaccaccgag 240
cggttcgcct gaaacgggcg ccggcgcggg tactgtcgcg actacccccc cgtcgtcgcc 300
ggtgacgttg gcggagaccg gtagcacgct gctctacccg ctgttcaacc tgggggtcc 360
ggcccttcac gagaggtatc cgaacgtcac gatcaccgct cagggcaccg gttctggtgc 420
cgggatcgcg caggccgcccgc ccgggacggt caacattggg gcctccgacg cctatctgtc 480
ggaaaggtat atggccgcgc acaaggggct gatgaacatc ggcgtagcca tctccgctca 540
gcaggtcaac tacaacctgc ccggagtgtag cgagcacctc aagctgaacg gaaaagtcc 600
ggcgccatg taccaggca ccatcaaaaac ctgggacgac cgcagatcg ctgcgtctaa 660
ccccggcgtg aacctgcccgc gcaccgcggt agtccgctg caccgcctcg acgggtccgg 720
tgacaccttc ttgttacccc agtacctgtc caagcaagat cccgagggt ggggcaagtc 780
gccccggcttc ggcaccaccg tcgacttccc ggcggtgccg ggtgcgttgg gtgagaacgg 840
caacggccgc atggtgcaccg gttgcgcga gacaccgggc tgcgtgcct atatcgcat 900
cagcttcctc gaccaggcca gtcaacgggg actcggcggag gccaactag gcaatagctc 960
tggcaatttc ttgttgcggc acgcgcaaa cattcaggcc gcggcgctg gttcgatc 1020
gaaaaccccg gcgaaccagg cgatttcgt gatcgacggg cccgcggcc acggctaccc 1080
gatcatcaac tacgagtacg ccatcgtaa caaccggcaa aaggacccg ccaccgcgca 1140
gaccctgcag gcatttctgc actgggcgtat caccgacggc aacaaggccct gttccctcg 1200
ccaggttcat ttccagccgc tgccgcccgc ggtgttgaag ttgtctgacg cggtgatc 1260
gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgtc gggccatc 1320
gctgcttgc ggagcatgct ggcggcgtcc ggtgaagtcg ggcgcgttgg cccggccatc 1380
cggtgggtgg gtggatagg tgcggtgatc ccgtctgttgc cgctggctt ggtgttgg 1440
gtgtgtgtca tcgaggcgat gggtgcgtat aggtcaacg gttgcattt cttcaccggc 1500
accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccac 1560
cggtcgccgc ctactacggg gcgttgcgc tgatcgctgg gacgctggcg acctcgccaa 1620
tgcgcctgtat catcgccgtg ccggctctgt taggagcggc gtcggtgatc gtggacggc 1680
tgccgaaacg gttggccgag gctgtggaa tagtccttggg attgctcgcc ggaatcccc 1740
gctgtgtcgat cggtttgtgg gggcaatgaa cgttcgggccc gttcatcgat catcacatcg 1800
ctccgggtat cgctcacaac gctcccgtat tgccgggtct gaaactacttgc ggcggccgacc 1860
cgggcaacgg ggagggcatg ttgtgttccg gtctgggttt ggcggtgatg gtcgttccca 1920
ttatcgccac caccactcat gacctgttcc ggcaggtgcc ggtgttggccc cgggagggcg 1980
cgatcgggaa ttc 1993

<210> 39
<211> 374
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> 38 kD

<400> 39
Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1 5 10 15
Leu Leu Leu Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20 25 30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35 40 45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50 55 60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65 70 75 80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85 90 95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100 105 110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115 120 125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130 135 140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145 150 155 160
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165 170 175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180 185 190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195 200 205
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
210 215 220
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
225 230 235 240
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
245 250 255
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
260 265 270
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
275 280 285
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
290 295 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

<210> 40
 <211> 999
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> DPEP

<400> 40
 atgcatcacc atcaccatca catgcatacg gtggaccca acttgacacg tcgcaaggga 60
 cgattggcgg cactggctat cgccggcgatg gccagcgcca gcctggtgac cgttgcgggt 120
 ccccgcgaccg ccaacgcccga tccggagccga gcgccccccgg taccacacaac ggccgcctcg 180
 ccggccgtcga ccgctgcagc gcccacccgca cggcgacac ctgttgcggcc cccaccacccg 240
 gccgcccggca acacgcccga tgcccagccg ggcgatccca acgcagcacc tcggccggcc 300
 gacccgaacg caccggccgc acctgtcatt gccccaaacg caccaccaacc tgcggatc 360
 gacaacccgg ttggaggatt cagcttcgctg ctgcctgctg gctgggtgga gtctgacgcc 420
 gcccacttcg actacggttc agcactcctc agcaaaaacca cgggggaccc gccatcccc 480
 ggacagccgc cgccgtggc caatgacacc cgtatgtgc tcggccggct agaccaaaag 540
 ctttacgcca gcgccgaagc caccgactcc aaggccggcgg cccgggtggg ctcggacatg 600
 ggtgagttct atatgcccta cccgggcacc cggatcaacc agggaaaccgt ctcgctcgac 660
 gccaacgggg tgcgttgcgtat tacgaagtca agttcagcga tccgagtaag 720
 ccgaacggcc agatctggac gggcgtaatc ggctcgcccg cggcgacgc accggacgcc 780
 gggcccccctc agcgctggtt tgcgttgcgtat ctcgggaccc ccaacaaccc ggtggacaag 840
 ggcgcggccca aggcgctggc cgaatcgatc cggcctttgg tcgccccggcc gccggcgccg 900
 gcaccggctc ctgcagagcc cgctccggcg cggcgcccg cggggaaagt cgctcctacc 960
 ccgacgacac cgacaccgca gcgaccccta cggcctga 999

<210> 41
 <211> 332
 <212> PRT
 <213> *Mycobacterium tuberculosis*

<220>
 <223> DPEP

<400> 41
 Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45

Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
50					55				60						
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
65					70			75			80				
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
			85					90					95		
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
			100					105					110		
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
			115					120				125			
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp
			130				135				140				
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro
	145				150				155				160		
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg
					165				170				175		
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala
					180				185				190		
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro
			195				200					205			
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val
	210				215				220						
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
	225				230				235				240		
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				245				250					255		
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
				260				265				270			
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu
				275			280				285				
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro	
	290				295				300						
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr		
	305				310				315				320		
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
				325				330							

<210> 42
 <211> 702
 <212> DNA
 <213> *Mycobacterium tuberculosis*

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<220>
<223> TbH4

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

<400> 42
cggcacgagg atcggtaccc cgccgcacatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcataat tagtgcagga accttcagt ttagcgacga taatggctat 180
agcactaagg aggtatgatcc gatatgacgc agtgcacac cgtgacggtg gatcagcaag 240
agatttgaa cagggccaac gaggtggagg ccccgatggc ggaccacccg actgtatgtcc 300
ccatcacacc gtgcgaactc acggngnta aaaacgcccgc ccaacagntg gtnttgcgtcc 360
ccgacaacat gcgggaaatac ctggcgcccg gtgccaaaga gcccgcgt ctggcgaccc 420
cgctgcgcaa cgccgccaag gngtatggcg aggttgcgtga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaaact gtgcaggcag aatcgccgg ggccgtcgaa ggggacagtt 540
cggccgaact aaccgatacg ccgagggtgg ccacggccgg tgaacccaac ttcatggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcatcgctc ggcactgng 660
ggatgggtg gaacacttnc accctgacgc tgcacaggcga cg 702

<210> 43
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

<400> 43
Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1           5           10          15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20          25           30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35           40          45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50           55          60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65           70          75          80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85           90          95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100          105          110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115          120          125

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Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
130														140	
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
145														155	160
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
														165	175
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
														180	190
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile
														195	205
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe
														210	220
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
														225	240
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
														245	255
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
														260	270
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Gly	Leu	Arg	Pro	Xaa	Lys		
														275	285

<210> 44
 <211> 339
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> DPPD genomic DNA

<400> 44
 atgaagttga agtttgctcg cctgagtaact gcgatactgg gttgtgcagc ggcgcgttgtg 60
 tttcctgcct cgggttgcag cgcagatcca cctgacccgc atcagccgga catgacgaaa 120
 ggctattgccc cgggtggccg atggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180
 taccggcggc gctcggtttt gcaccagttt atgcaaacgt ggtttaccgg cccacagttt 240
 tacttcgatt gtgtcagcgg cggtgagccc ctccccggcc cgccgcacc ggttggttgc 300
 ggtggggcaa ttccgtccga gcagcccaac gctccctga 339

<210> 45
 <211> 112
 <212> PRT
 <213> *Mycobacterium tuberculosis*

<220>
 <223> DPPD

<400> 45
 Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1 5 10 15

Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp
20						25					30				

Pro	His	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp
35					40						45				

Gly	Phe	Gly	Asp	Leu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly
50					55					60					

Ser	Phe	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe
65					70			75			80				

Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Leu	Pro	Gly	Pro	Pro	Pro
85						90					95				

Pro	Gly	Gly	Cys	Gly	Gly	Ala	Ile	Pro	Ser	Glu	Gln	Pro	Asn	Ala	Pro
100						105					110				

<210> 46
 <211> 921
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:tri-fusion
 protein DPV-MTI-MSL (designated MTb31F) cDNA

<220>
 <221> CDS
 <222> (1)..(900)
 <223> MTb31F

<400> 46																
cat	atg	cat	cac	cat	cac	cat	cat	gat	ccc	gtg	gac	gcg	gtc	att	aac	48
His	Met	His	His	His	His	His	His	Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	
1		5						10						15		
acc	acc	tgc	aat	tac	ggg	cag	gta	gta	gct	gcg	ctc	aac	gcg	acg	gat	96
Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp	
20				25							30					
ccg	ggg	gct	gcc	gca	cag	ttc	aac	gcc	tca	ccg	gtg	gcg	cag	tcc	tat	144
Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr	
35					40						45					
ttg	cgc	aat	ttc	ctc	gcc	gca	ccg	cca	cct	cag	cgc	gct	gcc	atg	gcc	192
Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	
50			55							60						
gcg	caa	ttg	caa	gct	gtg	ccg	ggg	gca	cag	tac	atc	ggc	ctt	gtc		240
Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val	
65				70					75				80			
gag	tcg	gtt	gcc	ggc	tcc	tgc	aac	aac	tat	gag	ctc	atg	acg	att	aat	288
Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Leu	Met	Thr	Ile	Asn	
85				90								95				
tac	cag	ttc	ggg	gac	gtc	gac	gct	cat	ggc	gcc	atg	atc	cgc	gct	cag	336
Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	
100					105						110					

gct gct tcg ctt gag gct gag cat cag gcc atc gtt cgt gat gtg ttg Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu 115 120 125	384
gcc gct ggt gac ttt tgg ggc ggc gct tcg gtg gct tgc cag gag Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu 130 135 140	432
ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala 145 150 155 160	480
aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gct caa Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln 165 170 175	528
acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu 180 185 190	576
gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gct ttt gcc gcc Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala 195 200 205	624
aag gct ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gct gct Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala 210 215 220	672
atg tcg gct cag gct ttt cac cag ggg gag tcg tcg gct gct ttt cag Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln 225 230 235 240	720
gcc gcc cat gcc cgg ttt gtg gct gct gcc gcc aaa gtc aac acc ttg Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu 245 250 255	768
ttg gat gtc gct cag gct aat ctg ggt gag gcc gct ggt acc tat gtg Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val 260 265 270	816
gcc gcc gat gct gct gct gct tcg acc tat acc ggg ttc gat atc cat Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His 275 280 285	864
cac act ggc ggc cgc tcg agc aga tcc ggc tgc taa caaagcccgaa His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys 290 295 300	910
aaggaagctg a	921

<210> 47
 <211> 299
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tri-fusion
 protein DPV-MTI-MSL (designated MTb31F) cDNA

<400> 47
 His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 5 10 15

Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp
				20				25					30		
Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr
				35				40					45		
Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala
				50				55				60			
Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val
				65				70			75		80		
Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Leu	Met	Thr	Ile	Asn
				85				90					95		
Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
				100				105				110			
Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu
				115				120				125			
Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu
				130				135				140			
Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala
				145				150			155		160		
Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln
				165				170					175		
Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu
				180				185				190			
Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala
				195				200				205			
Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala
				210				215				220			
Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln
				225				230			235		240		
Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	
				245				250				255			
Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val
				260				265				270			
Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	Phe	Asp	Ile	His
				275				280				285			
His	Thr	Gly	Gly	Arg	Ser	Ser	Arg	Ser	Gly	Cys					
				290				295							

<210> 48
 <211> 2168
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:tetra-fusion
      protein DPV-MTI-MSL-MTCC#2 (designated MTb71F)

<220>
<221> CDS
<222> (1)..(2133)
<223> MTb71F

<400> 48
cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
  1           5           10           15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
  20          25          30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
  35          40          45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
  50          55          60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
  65          70          75          80

gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
  85          90          95

tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag 336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
  100         105         110

gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg 384
Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
  115         120         125

gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag 432
Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
  130         135         140

ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc 480
Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
  145         150         155         160

aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa 528
Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
  165         170         175

acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg 576
Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
  180         185         190

gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc 624
Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
  195         200         205

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aag gcg ggg ctg atg cg	cac acg atc ggt cag	gcc gag cag gcg gcg	672
Lys Ala Gly Leu Met Arg	His Thr Ile Gly Gln	Ala Glu Gln Ala Ala	
210	215	220	
atg tcg gct cag gcg ttt	cac cag ggg gag tcg	tcg gcg gcg ttt cag	720
Met Ser Ala Gln Ala	Phe His Gln Gly Glu	Ser Ser Ala Ala Phe Gln	
225	230	235	240
gcc gcc cat gcc cg	ttt gtg gcg gcg gcc	gcc aaa gtc aac acc tt	768
Ala Ala His Ala Arg	Phe Val Ala Ala Ala	Lys Val Asn Thr Leu	
245	250	255	
ttg gat gtc gcg cag	gct gcg aat ctg ggt gag	gcc gcc ggt acc tat gt	816
Leu Asp Val Ala Gln	Ala Asn Leu Gly Glu	Ala Ala Gly Thr Tyr Val	
260	265	270	
gcc gcc gat gct gcg	gcc gcg tcg acc tat acc	ggg ttc gat atc atg	864
Ala Ala Asp Ala Ala	Ala Ser Thr Tyr Thr	Gly Phe Asp Ile Met	
275	280	285	
gat ttc ggg ctt tta	cct ccg gaa gtg aat tca	agc cga atg tat tcc	912
Asp Phe Gly Leu Leu	Pro Pro Glu Val Asn	Ser Ser Arg Met Tyr Ser	
290	295	300	
ggg ccg ggg ccg gag	tcg atg cta gcc gcc gcg	gcc gcc tgg gac ggt	960
Gly Pro Gly Pro Glu	Ser Met Leu Ala Ala	Ala Ala Ala Trp Asp Gly	
305	310	315	320
gtg gcc gcg gag tt	g act tcc gcc gct tcg	tat gga tcg gtg gtg	1008
Val Ala Ala Glu Leu	Thr Ser Ala Ala Val	Ser Tyr Gly Ser Val Val	
325	330	335	
tcg acg ctg atc gtt	gag ccg tgg atg ggg ccg	gct gcg gct gct atg	1056
Ser Thr Leu Ile Val	Glu Pro Trp Met Gly	Pro Ala Ala Ala Ala Met	
340	345	350	
gct gcc gct gca acg	ccg tat gtg ggg tgg ctg	gcc gcc acg gct gct	1104
Ala Ala Ala Ala Thr	Pro Tyr Val Gly Trp	Leu Ala Ala Thr Ala Ala	
355	360	365	
ctg gct aag gag acg	gcc aca cag gct agg	gca gct gct gct gct	1152
Leu Ala Lys Glu Thr	Ala Thr Gln Ala Arg	Ala Ala Glu Ala Phe	
370	375	380	
ggg acg gct ttc gct	atg acg gtg cca cca	tcc ctc gtc gct gcc aac	1200
Gly Thr Ala Phe Ala	Met Thr Val Pro Pro	Ser Leu Val Ala Ala Asn	
385	390	395	400
cgc agc cgg ttg atg	tcg ctg gtc gct gct	aac att ctg ggg caa aac	1248
Arg Ser Arg Leu Met	Ser Leu Val Ala Ala	Asn Ile Leu Gly Gln Asn	
405	410	415	
agt gct gct atc gct	acc cag gcc gag tat	gcc gaa atg tgg gcc	1296
Ser Ala Ala Ile Ala	Thr Gln Ala Glu Tyr	Ala Glu Met Trp Ala	
420	425	430	
caa gac gct gcc gt	tg atg tac agc tat gag	ggg gca tct gct gct gct	1344
Gln Asp Ala Ala Val	Met Tyr Ser Tyr Glu	Gly Ala Ser Ala Ala Ala	
435	440	445	

tcg gcg ttg ccg ccg ttc act cca ccc gtg caa ggc acc ggc ccg gcc Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala 450 455 460	1392
ggg ccc gcg gcc gca gcc gcg acc caa gcc gcc ggt gcg ggc gcc Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala 465 470 475 480	1440
gtt gcg gat gca cag gcg aca ctg gcc cag ctg ccc ccg ggg atc ctg Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu 485 490 495	1488
agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg aca tcg Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser 500 505 510	1536
gga ctg ttg ggg atc gcg tcg acc ctc aac ccg caa gtc gga tcc gct Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala 515 520 525	1584
cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala 530 535 540	1632
ctc tac att gca tcc atc gcg acc ggc agc att gcg ctc gcg atc acg Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr 545 550 555 560	1680
aac acg gcc aga ccc tgg cac atc ggc cta tac ggg aac gcc ggc ggg Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly 565 570 575	1728
ctg gga ccg acg cag ggc cat cca ctg agt tcg gcg acc gac gag ccg Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro 580 585 590	1776
gag ccg cac tgg ggc ccc ttc ggg ggc gcg gcg ccg gtg tcc gcg ggc Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly 595 600 605	1824
gtc ggc cac gca gca tta gtc gga gcg ttg tcg gtg ccg cac agc tgg Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp 610 615 620	1872
acc acg gcc gcc ccg gag atc cag ctc gcc gtt cag gca aca ccc acc Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr 625 630 635 640	1920
ttc agc tcc agc gcc ggc gac ccg acg gcc cta aac ggg atg ccg Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro 645 650 655	1968
gca ggc ctg ctc agc ggg atg gct ttg gcg agc ctg gcc gca cgc ggc Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly 660 665 670	2016
acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln 675 680 685	2064

gag gac ggc cgc aaa ccc ccc gta gtt gtg att aga gag cag ccg ccg 2112
Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
690 695 700

ccc gga aac ccc ccc cggtaa gatttctaaa tccatcacac tggcggccgc 2163
Pro Gly Asn Pro Pro Arg
705 710

tcgag 2168

<210> 49
<211> 710
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:tetra-fusion
protein DPV-MTI-MSL-MTCC#2 (designated MTb71F)

<400> 49
His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
20 25 30

Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
35 40 45

Leu Arg Asn Phe Leu Ala Ala Pro Pro Gln Arg Ala Ala Met Ala
50 55 60

Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
65 70 75 80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
85 90 95

Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
100 105 110

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
115 120 125

Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
130 135 140

Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
145 150 155 160

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
165 170 175

Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
180 185 190

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
195 200 205

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
210 215 220

Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
225 230 235 240

Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu
245 250 255

Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
260 265 270

Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met
275 280 285

Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser
290 295 300

Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly
305 310 315 320

Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val
325 330 335

Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met
340 345 350

Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala
355 360 365

Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe
370 375 380

Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn
385 390 395 400

Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn
405 410 415

Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala
420 425 430

Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala
435 440 445

Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala
450 455 460

Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala
465 470 475 480

Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu
485 490 495

Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser
500 505 510

Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala
515 520 525

Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala
530 535 540

Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
 545 550 555 560
 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
 565 570 575
 Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
 580 585 590
 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
 595 600 605
 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
 610 615 620
 Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
 625 630 635 640
 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655
 Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
 660 665 670
 Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
 675 680 685
 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
 690 695 700
 Pro Gly Asn Pro Pro Arg
 705 710

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 <211> 588
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> Ra35 N-terminus of MTB32A (Ra35FL)

<400> 50
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 aacaacgccc tggccgcgg gaccggcatc gtcatcgatc ccaacgggtgt cgtgctgacc 180
 aacaaccacg tgatcgccgg cgccaccgac atcaatgcgt tcagcgctgg ctccggccaa 240
 acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgccgt gctgcagctg 300
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